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1 25
MDINASRALANVYDLPDDFFPKIDDLVRDAKDALEPYWR

50 75
SDSIKKHVLIATHFVDLIEDFWQTTQGMHEIAEALRAVI

100
PPTTTPVPAGYLIQHEEAEEIPLGDLFKHQEERIVSFQP

125 150
DYPITARIHAHLKAYAKINEESLDRARRLLWWHYNCLLW

175
GEANVTNYISRLRTWLSTPERYRGRDAPTIEAITRPIQV

200 225
AQGGRKTSSGTRKPRGLEPRRRKVKTTVVYGRRRSKSRD

250 262
RRAPSPQRAGSPLPRSSSSHRRSPSPRK

FIG. 1



NUCLEIC ACID SEQUENCE OF DUCK HEPATITIS B CORE PROTEIN

1 50
ATGGATATCAATGCTTCTAGAGCCTTAGCCAATGTTTATGATTGGCCAGATGATTTCTTCCC

100
AAAAATTGATGATCTTGTAAGGGATGCGAAGGATGCTTTAGAACCTTATTGGAGATCAGATT

150
CAATAAAGAAACATGTTTTAATTGCAACTCACTTTGTGGATCTTATTGAAGACTTCTGGCAA

200
ACTACTCAGGGTATGCATGAAATAGCTGAAGCCTTAAGAGCAGTTATACCACCTACTACAAC

250 300
ACCAGTTCCCGCAGGATATCTGATTGAGCAGCAAGAGGCTGAGGAGATTCTCTGGGAGATT

350
TATTTAAACATCAGGAAGAAAGGATAGTTAGTTTCCAACCGGATTATCCTATTACTGCACGA

400
ATTCATGCACACCTGAAAGCTTATGCAAAGATTAACGAGGAATCACTGGATAGGGCTAGGAG

450
ATTGCTTTGGTGGCATTACAATTGTTTACTGTGGGGAGAAGCTAACGTTACTAATTATATTT

500 550
CTCGGCTTCGCACTTGGCTATCAACACCTGAGAGATACAGAGGCCGAGATGCCCCAACCAT

600
GAAGCAATCACTAGACCAATCCAAGTGGCTCAGGGAGGCAGAAAAACATCTTCGGGTACTAG

650
AAAACCTCGTGGACTCGAACCTAGAAGAAGAAAGTTAAAACCACAGTTGTCTATGGGAGAA

700
GACGTTCAAAGTCCAGGGATAGGAGAGCCCCTTACCCCCAACGTGCGGGCTCCCCTCTCCCG

750 786
CGTAGTTGAGCAGCCACAGAAGATCTCCCTCGCCTAGGAAA

FIG. 2

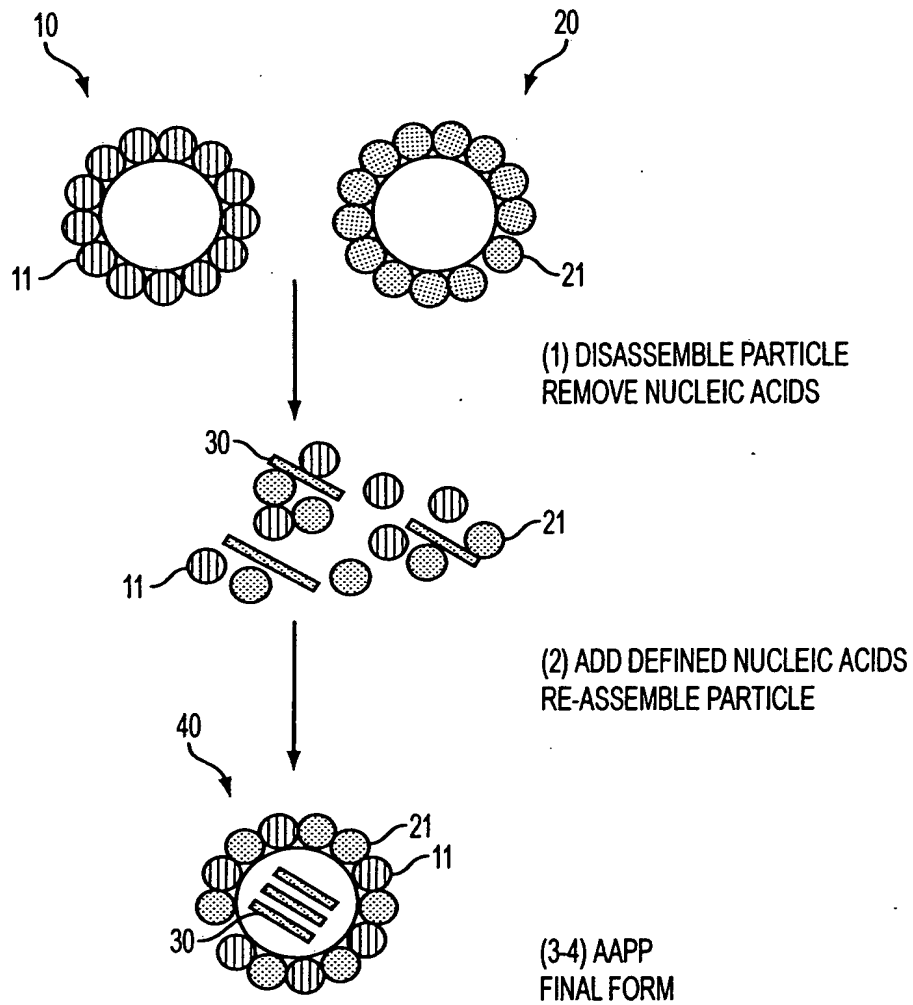


FIG. 3

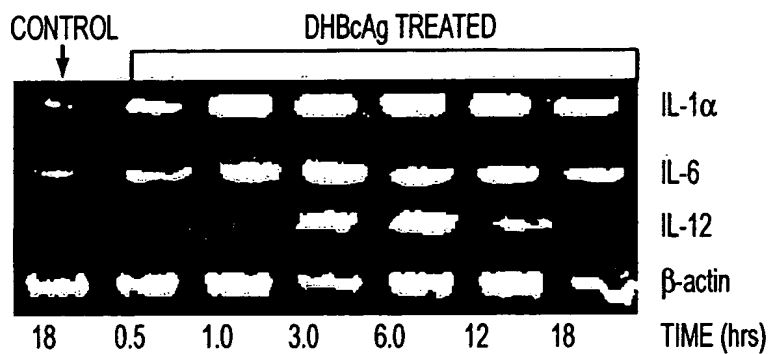


FIG. 4A

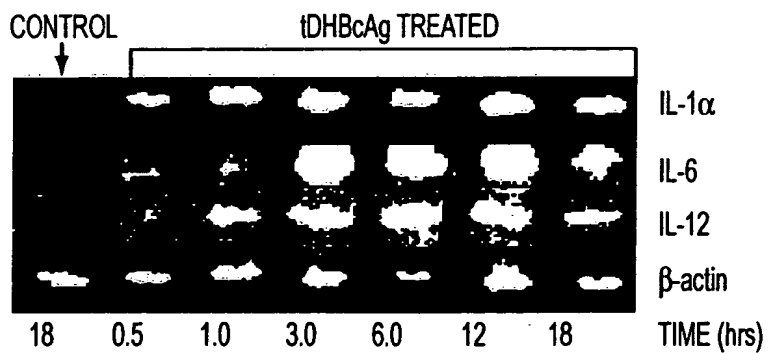


FIG. 4B

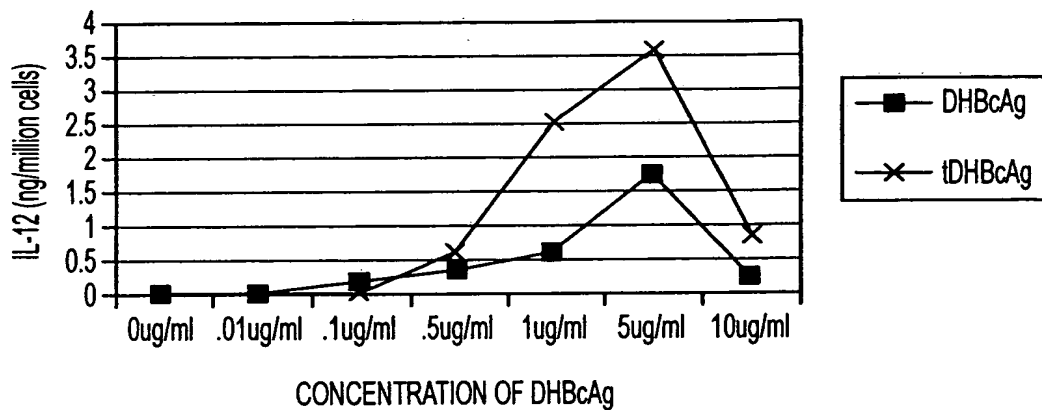


FIG. 5A

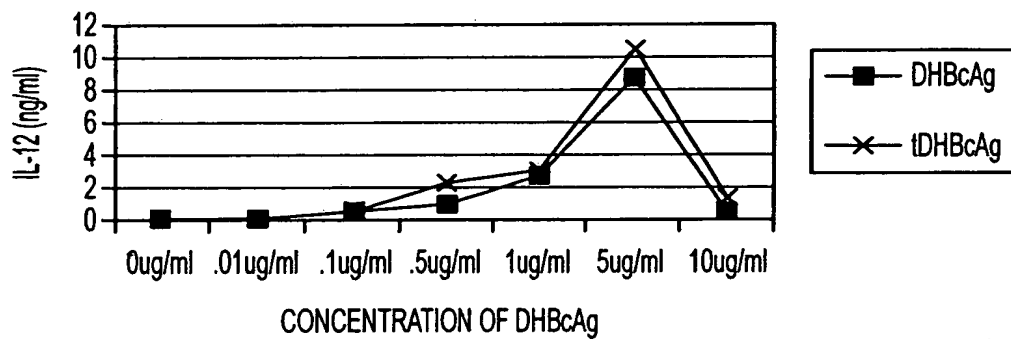


FIG. 5B

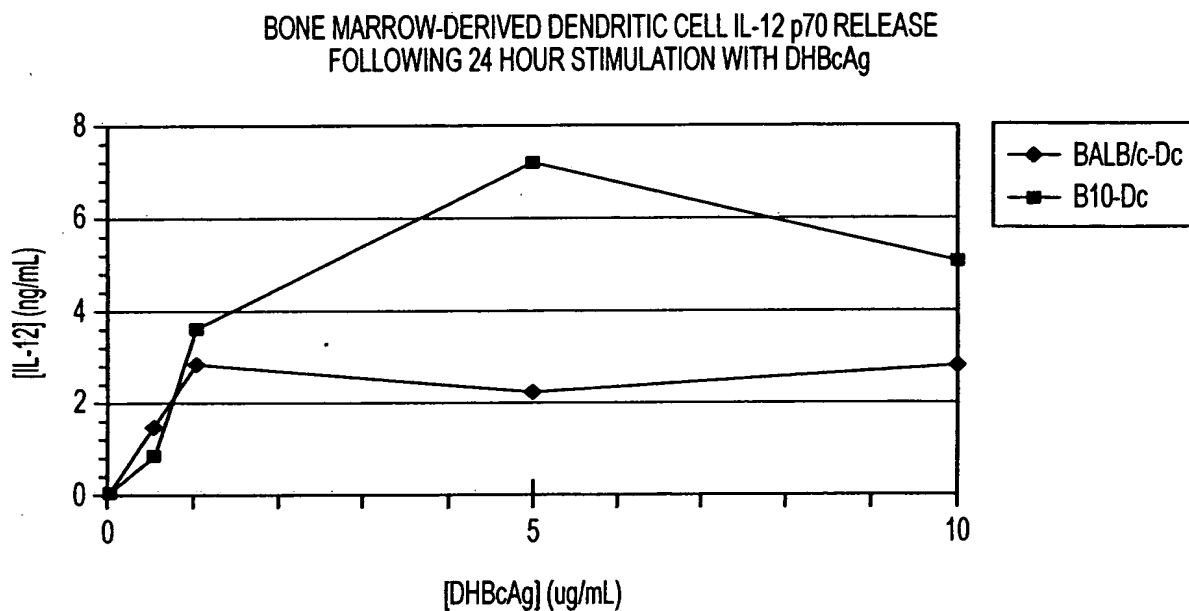


FIG. 6

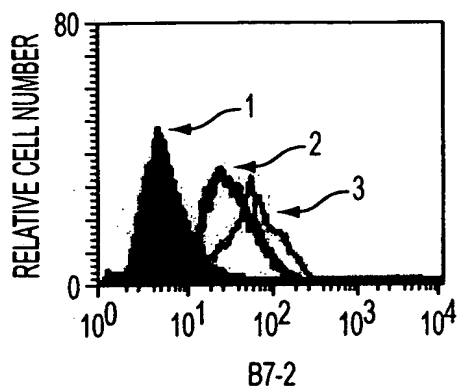


FIG. 7A

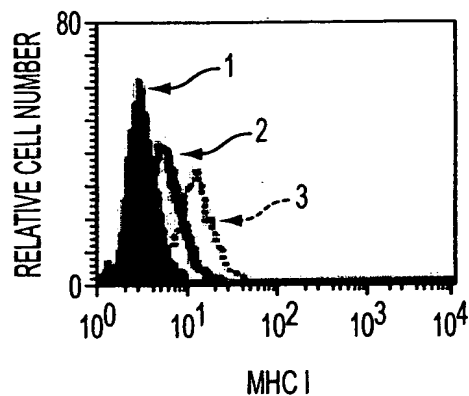


FIG. 7B

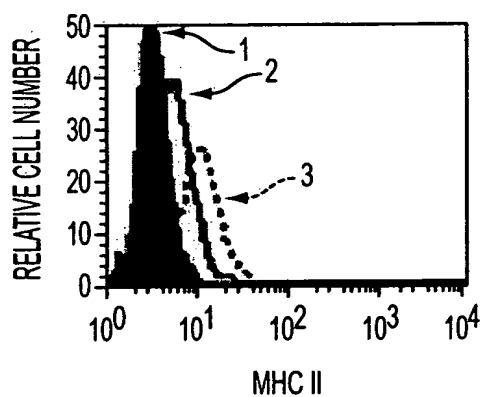


FIG. 7C

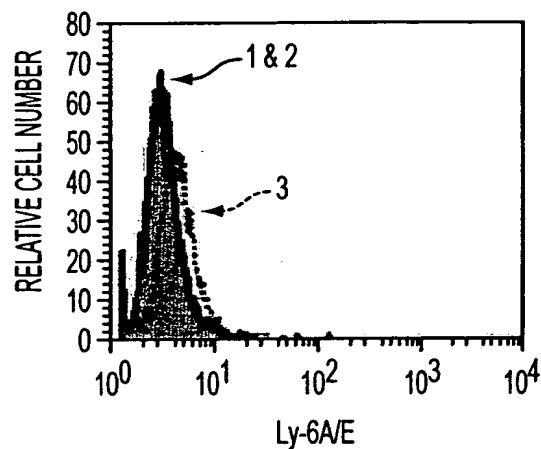


FIG. 7D

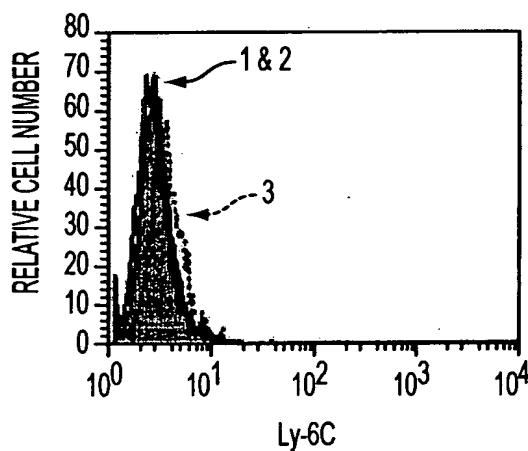


FIG. 7E

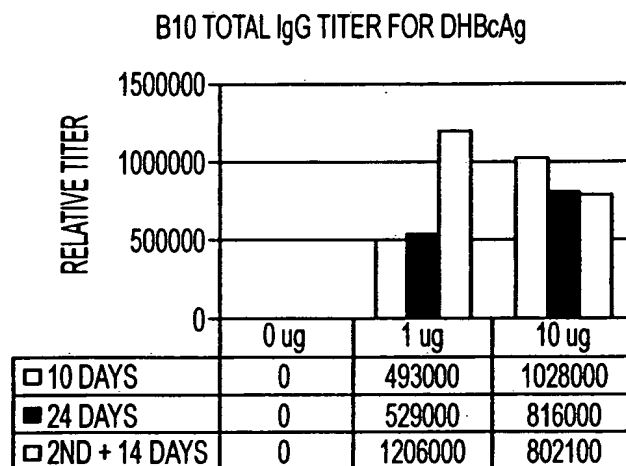


FIG. 8A

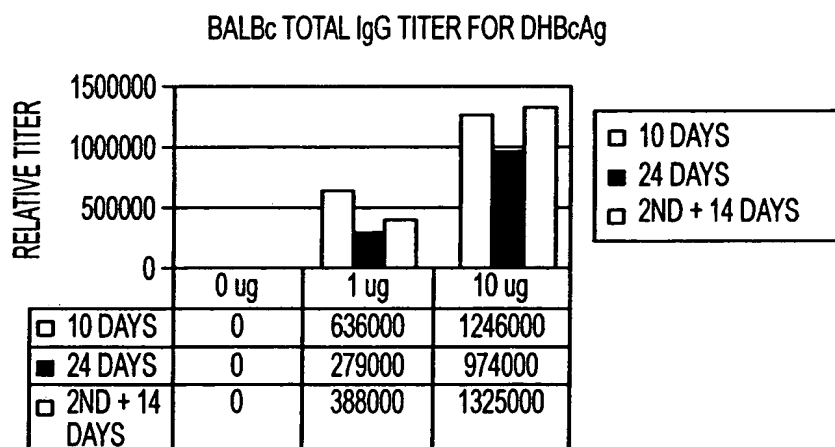


FIG. 8B

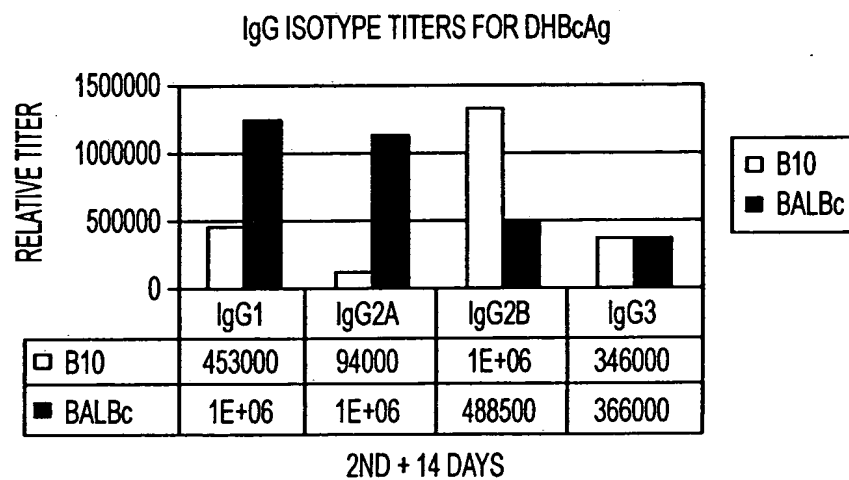


FIG. 9

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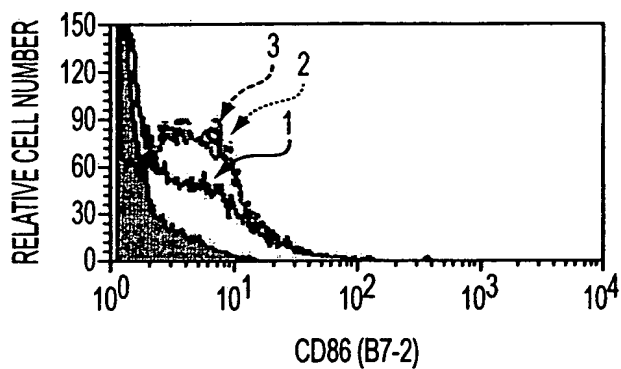


FIG. 10A

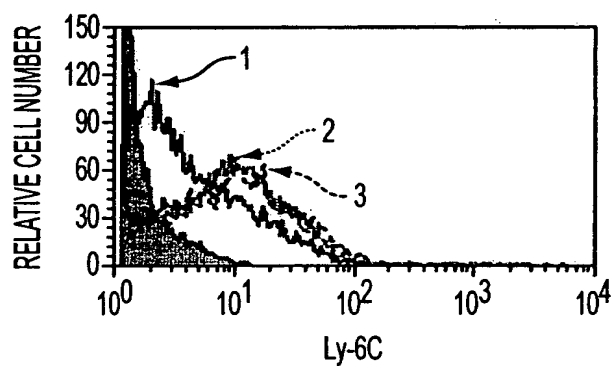


FIG. 10B

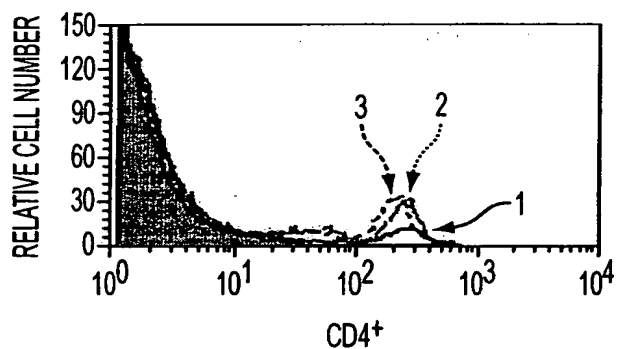


FIG. 10C

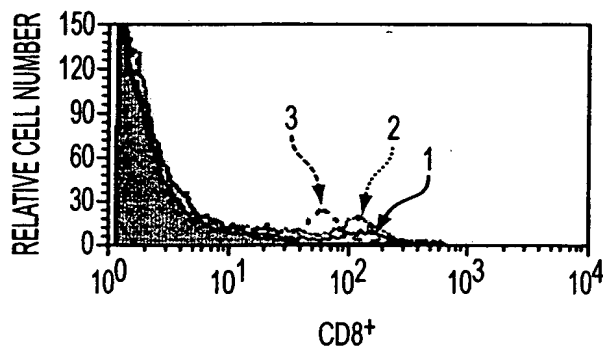


FIG. 10D

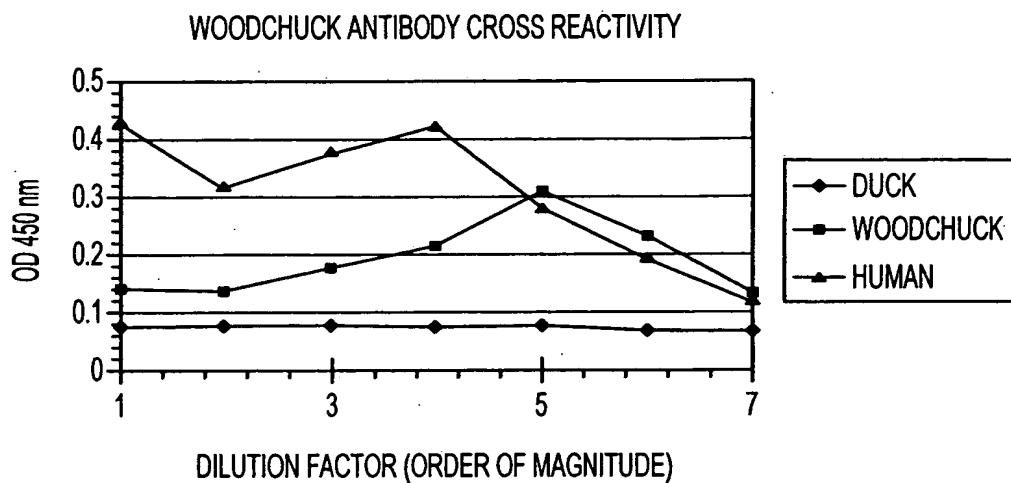


FIG. 11A

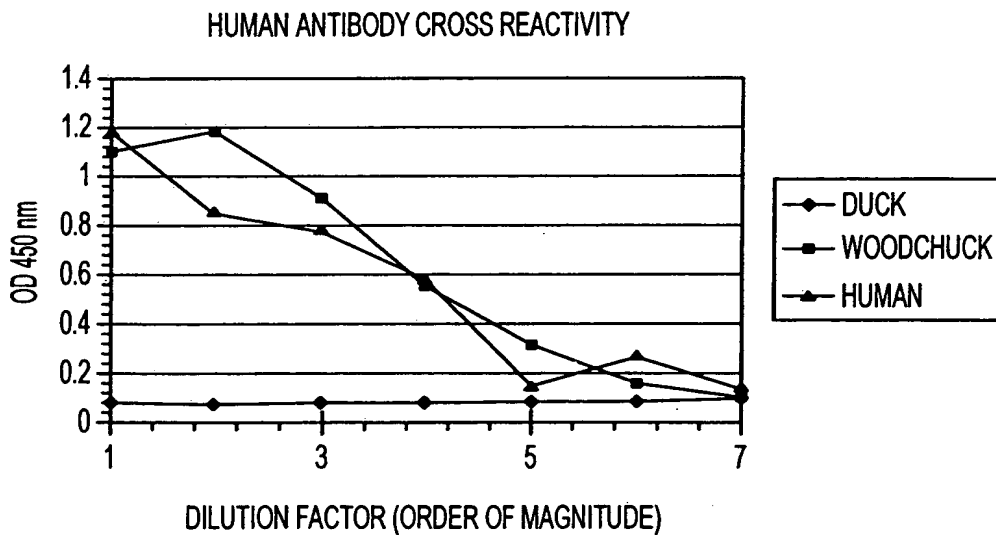
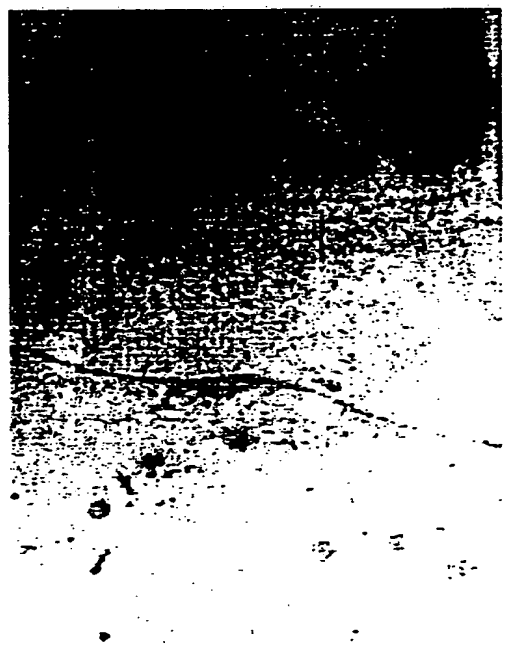


FIG. 11B



1 2 3 4



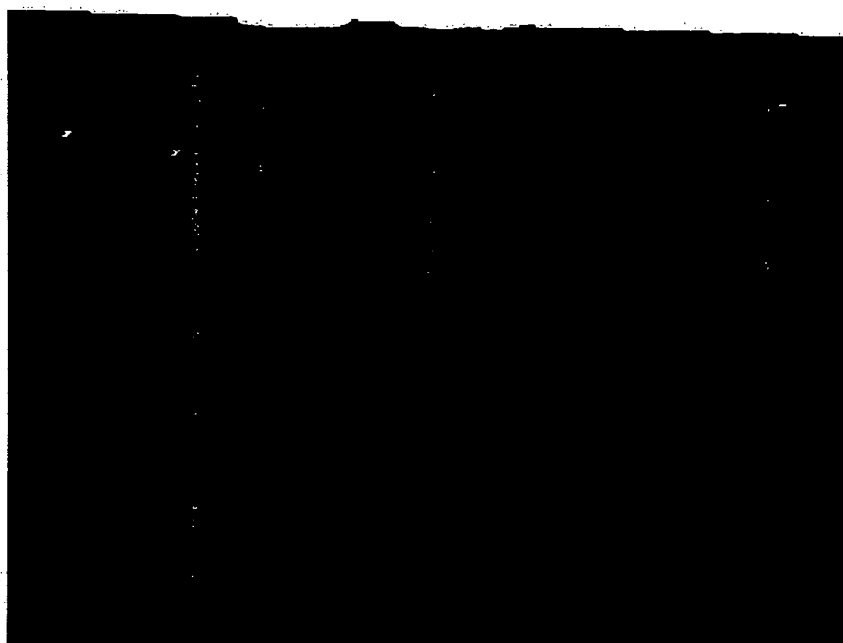
← DUCK HBcAg

FIG. 12

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Inventor: Darrell Peterson
Title: ADVANCED ANTIGEN
PRESENTATION PLATFORM
Attorney Docket No. 48507-00002
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1 2 3 4 5



← DUCK HBcAg

FIG. 13

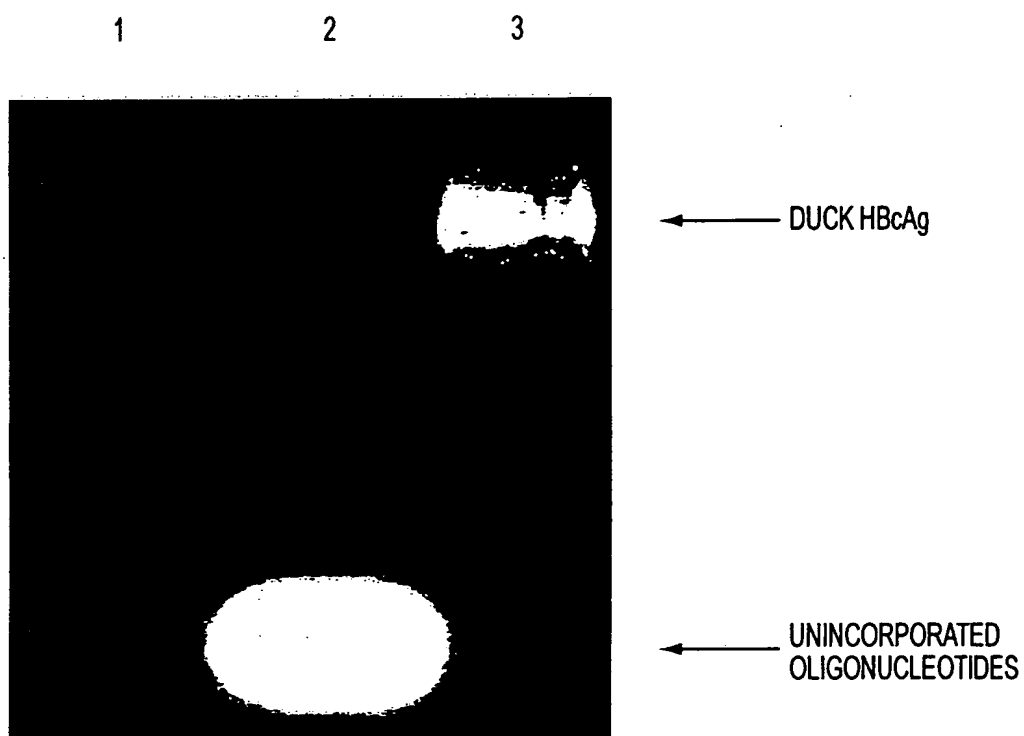


FIG. 14

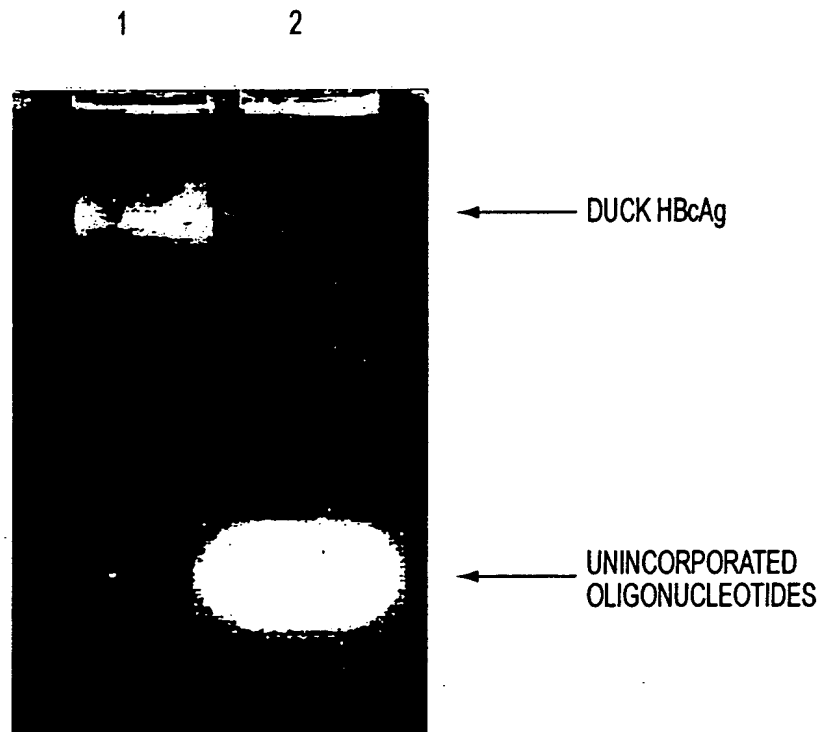


FIG. 15

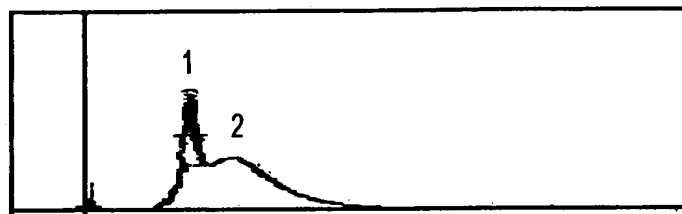


FIG. 16A

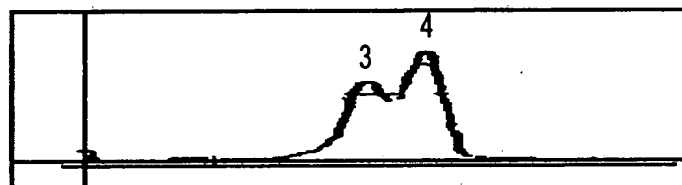


FIG. 16B

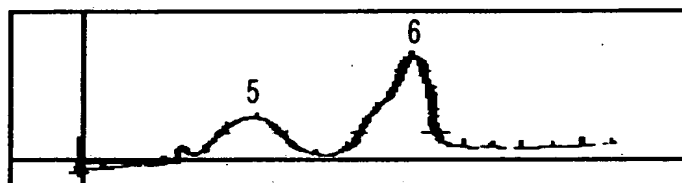


FIG. 16C

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AMINO ACID SEQUENCE OF DUCK HEPATITIS B CORE PROTEIN MUTANT 1-239

1 25
MDINASRALANVYDLPDDEFKIDDLVRDAKDALEPYWR
50 75
SDSIKKHVLIATHFVDLIEDFWQTTQGMHEIAEALRAVI
100
PPTTTPVPAGYLIQHEEAEIPLGDLFKHQEERIVSFQP
125 150
DYPITARIHAHLKAYAKINEESLDRARRLLWWHYNCLLW
175
GEANVTNYISRLRTLWLSTPERYRGRDAPTIEAITRPIQV
200 225
AQGGRKTSSGTRKPRGLEPRRRKVKT TVVYGRRRSKSRD
239
RRAPS

FIG.17



NUCLEIC ACID SEQUENCE OF DUCK HEPATITIS B CORE PROTEIN MUTANT 1-239

1 50
ATGGATATCAATGCTTCTAGAGCCTTAGCCAATGTTTATGATTGCCAGATGATTTCTTCCC

100
AAAAATTGATGATCTTGTAAGGGATGCGAAGGATGCTTTAGAACCTTATTGGAGATCAGATT

150
CAATAAAGAAACATGTTTTAATTGCAACTCACTTTGTGGATCTTATTGAAGACTTCTGGCAA

200
ACTACTCAGGGTATGCATGAAATAGCTGAAGCCTTAAGAGCAGTTATACCACCTACTACAAC

250 300
ACCAGTTCCCGCAGGATATCTGATT CAGCACGAAGAGGCTGAGGAGATTCCTCTGGGAGATT

350
TATTTAAACATCAGGAAGAAAGGATAGTTAGTTTCCAACCGGATTATCCTATTACTGCACGA

400
ATTCATGCACACCTGAAAGCTTATGCAAAGATTAACGAGGAATCACTGGATAGGGCTAGGAG

450
ATTGCTTTGGTGGCATTACAATTGTTTACTGTGGGGAGAAGCTAACGTTACTAATTATATTT

500 550
CTCGGCTTCGCACTTGGCTATCAACACCTGAGAGATACAGAGGCCGAGATGCCCCAACCATT

600
GAAGCAATCACTAGACCAATCCAAGTGGCTCAGGGAGGCAGAAAAACATCTTCGGGTACTAG

650
AAAACCTCGTGGACTCGAACCTAGAAGAAGAAAAGTTAAAACCACAGTTGTCTATGGGAGAA

700 718
GACGTTCAAAGTCCAGGGATAGGAGAGCCCCTTCA

FIG. 18



AMINO ACID SEQUENCE OF TRUNCATED DUCK HEPATITIS B CORE PROTEIN

1 25
MDINASRALANVYDLPPDDFFPKIDDLVRDAKDALEPYWR

50 75
SDSIKKHVLIATHFVDLIEDFWQTTQGMHEIAEALRAVI

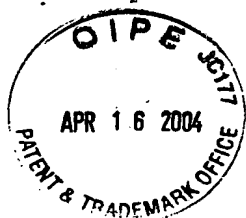
100
PPTTTPVPAGYLIQHEEAEEIPLGDLFKHQEERIVSFQP

125 150
DYPITARIHAHLKAYAKINEESLDRARRLLWWHYNCLLW

175
GEANVTNYISRLRTLSTPERYRGRDAPTIEAITRPIQV

200 214
AQGGRKTSSGTRKPRGLEP

FIG. 19



NUCLEIC ACID SEQUENCE OF TRUNCATED DUCK HEPATITIS B CORE PROTEIN

1 50
ATGGATATCAATGCTTCTAGAGCCTTAGCCAATGTTTATGATTTGCCAGATGATTTCTTCCC
100
AAAAATTGATGATCTTGTAAGGGATGCGAAGGATGCTTTAGAACCTTATTGGAGATCAGATT
150
CAATAAAGAAACATGTTTTAATTGCAACTCACTTTGTGGATCTTATTGAAGACTTCTGGCAA
200
ACTACTCAGGGTATGCATGAAATAGCTGAAGCCTTAAGAGCAGTTATACCACCTACTACAAC
250 300
ACCAGTTCCCGCAGGATATCTGATTCAGCACGAAGAGGCTGAGGAGATTCCTCTGGGAGATT
350
TATTTAAACATCAGGAAGAAAGGATAGTTAGTTTCCAACCGGATTATCCTATTACTGCACGA
400
ATTCATGCACACCTGAAAGCTTATGCAAAGATTAACGAGGAATCACTGGATAGGGCTAGGAG
450
ATTGCTTTGGTGGCATTACAATTGTTTACTGTGGGGAGAAGCTAACGTTACTAATTATATTT
500 550
CTCGGCTTCGCACTTGGCTATCAACACCTGAGAGATACAGAGGCCGAGATGCCCCAACCATT
600
GAAGCAATCACTAGACCAATCCAAGTGGCTCAGGGAGGCAGAAAAACATCTTCGGGTACTAG
642
AAAACCTCGTGGACTCGAACCT

FIG. 20